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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,412

DATE: 10/18/2001
TIME: 09:43:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\10182001\I964412.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: de la Monte, Suzanne
7 Wands, Jack R.
9 (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
10 Screening Drugs Effective for the Treatment or Prevention
11 of Alzheimer's Disease
13 (iii) NUMBER OF SEQUENCES: 14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
17 (B) STREET: 1100 New York Ave., Suite 600
18 (C) CITY: Washington
19 (D) STATE: DC
20 (E) COUNTRY: USA
21 (F) ZIP: 20005-3934
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/964,412
C--> 31 (B) FILING DATE: 28-Sep-2001.
32 (C) CLASSIFICATION:
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Esmond, Robert W.
36 (B) REGISTRATION NUMBER: 32,893
37 (C) REFERENCE/DOCKET NUMBER: 0609.4370000
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 202-371-2600
41 (B) TELEFAX: 202-371-2540
44 (2) INFORMATION FOR SEQ ID NO: 1:
46 (i) SEQUENCE CHARACTERISTICS:
47 (A) LENGTH: 1442 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: double
50 (D) TOPOLOGY: both
52 (ii) MOLECULE TYPE: cDNA
55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 15..1139
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63 TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC 50
64 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
65 1 5 10
67 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC 98
68 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser

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69	15	20	25	
71	GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC	146		
72	Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys			
73	30 35 40			
75	ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT	194		
76	Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe			
77	45 50 55 60			
79	CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC	242		
80	Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro			
81	65 70 75			
83	TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC	290		
84	Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala			
85	80 85 90			
87	CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG	338		
88	Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met			
89	95 100 105			
91	TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC	386		
92	Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu			
93	110 115 120			
95	CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT	434		
96	Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile			
97	125 130 135 140			
99	TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG	482		
100	Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val			
101	145 150 155			
103	CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG	530		
104	Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys			
105	160 165 170			
107	CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC	578		
108	His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His			
109	175 180 185			
111	CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG	626		
112	His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln			
113	190 195 200			
115	AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC	674		
116	Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly			
119	205 210 215 220			
121	TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC	722		
122	Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser			
123	225 230 235			
125	CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT	770		
126	Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe			
127	240 245 250			
129	TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC	818		
130	Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile			
131	255 260 265			
133	TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT	866		
134	Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala			
135	270 275 280			

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137 GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT      914
138 Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys
139 285                      290                      295                      300
141 TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG      962
142 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp
143                      305                      310                      315
145 CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC      1010
146 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
147                      320                      325                      330
149 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA      1058
150 Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro
151                      335                      340                      345
153 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT      1106
154 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
155                      350                      355                      360
157 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT      1159
158 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
159 365                      370                      375
161 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA      1219
163 AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT      1279
165 CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTTA AACAGTTACA      1339
167 TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA      1399
169 GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA                      1442
172 (2) INFORMATION FOR SEQ ID NO: 2:
174     (i) SEQUENCE CHARACTERISTICS:
175         (A) LENGTH: 375 amino acids
176         (B) TYPE: amino acid
177         (D) TOPOLOGY: linear
181     (ii) MOLECULE TYPE: protein
183     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
185 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
186  1                      5                      10                      15
188 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
189                      20                      25                      30
191 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
192                      35                      40                      45
194 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
195                      50                      55                      60
197 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
198  65                      70                      75                      80
200 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
201                      85                      90                      95
203 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
204                      100                     105                     110
206 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
207                      115                     120                     125
209 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
210                      130                     135                     140
212 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp

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213	145				150					155				160		
215	His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	His	Pro	Pro	Ala
216					165					170					175	
218	Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	His	Tyr	Thr	Trp
219				180					185					190		
221	Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln	Ser	Leu	Asn	Ser
222			195					200					205			
224	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly	Ser	Leu	Gln	Pro
225		210					215					220				
227	Leu	Pro	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser	Leu	Leu	Ser	Ser
228	225					230					235				240	
230	Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe	Phe	Val	Phe	Leu
231				245					250					255		
233	Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	Leu	Ile	Ser	Gly
234			260						265					270		
237	Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Gly	Ile	Thr	Gly
238		275					280					285				
240	Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys	Leu	Phe	Glu	Met
241		290				295					300					
243	Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Pro	Asn	Leu	Gly
244	305				310				315					320		
246	Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe	Ser	Cys	Leu	Ser
247			325						330					335		
249	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His	Leu	Pro	Pro	His	Pro	Ala	Asn
250			340					345					350			
252	Phe	Cys	Ile	Phe	Ile	Arg	Gly	Gly	Val	Ser	Pro	Tyr	Leu	Ser	Gly	Trp
253		355				360						365				
255	Ser	Gln	Thr	Pro	Asp	Leu	Arg									
256		370				375										

258 (2) INFORMATION FOR SEQ ID NO: 3:

260 (i) SEQUENCE CHARACTERISTICS:

261 (A) LENGTH: 1381 base pairs

262 (B) TYPE: nucleic acid

263 (C) STRANDEDNESS: double

264 (D) TOPOLOGY: both

266 (ii) MOLECULE TYPE: cDNA

271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

273	TTTTTTTTTT	GAGATGGAGT	TTTCGCTCTT	GTTGCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
275	CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
277	AGTAGCTGGG	ATTACAGGCA	TGTGCACCAC	GCTCGGCTAA	TTTGTATTT	TTTTTTAGTA	180
279	GAGATGGAGT	TTAACTCCAT	GTTGGTCAGG	CTGGTCTCGA	ACTCCCGACC	TCAGATGATC	240
281	TCCCGTCTCG	GCCTGCCCAA	AGTGCTGAGA	TTACAGGCAT	GAGCCACCAT	GCCCGGCCTC	300
283	TGCCTGGCTA	ATTTTGTGG	TAGAAACAGG	GTTTCACTGA	TGTTGCCCAA	GCTGGTCTCC	360
285	TGAGCTCAAG	CAGTCCACCT	GCCTCAGCCT	CCCAAAGTGC	TGGGATTACA	GGCGTCAGCC	420
287	GTGCCTGGCC	TTTTTATTTT	ATTTTTTTTA	AGACACAGGT	GTACCACTCT	TACCCAGGAT	480
289	GAAGTGCAGT	GGTGTGATCA	CAGCTCACTG	CAGCCTTCAA	CTCCTGAGAT	CAAGCAATCC	540
291	TCCTGCCTCA	GCCTCCCAAG	TAGCTGGGAC	CAAAGACATG	CACCACTACA	CCTGGTAATT	600
293	TTTATTTTTA	TTTTTAATTT	TTTGAGACAG	AGTCTCACTC	TGTCACCCAG	GCTGGAGTGC	660
296	AGTGGCGCAA	TCTTGGCTCA	CTGCAACCTC	TGCCTCCCGG	GTTCAAGTTA	TTCTCCTGCC	720

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298 CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTTGTAT 780
300 TTTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTGA TCTTGATCTC TTGACCTTGT 840
302 GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC 900
304 CTATTTTAA TTTTGTGTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
306 AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC 1020
308 AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT 1080
310 CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCCTGA CCTCAGGTGA 1140
312 CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
314 GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
316 TCAAACCTTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320
318 TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380
320 C 1381

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322 (2) INFORMATION FOR SEQ ID NO: 4:

324 (i) SEQUENCE CHARACTERISTICS:

325 (A) LENGTH: 1418 base pairs

326 (B) TYPE: nucleic acid

327 (C) STRANDEDNESS: both

328 (D) TOPOLOGY: both

330 (ii) MOLECULE TYPE: cDNA

335 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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337 TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT 60
339 CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
341 AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT 180
343 AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT 240
345 CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCC GCCTCTGCCT 300
347 GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT 360
349 CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC 420
351 TGGCCTTTTT ATTTTATTTT TTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480
355 GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540
357 TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTAT 600
359 TTTTATTTTT AATTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660
361 GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG 720
363 CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGTATTTTT 780
365 AGTAGAGATG GGGTTTCACC ATGTTGCCA GGTTGATGCT AGATCTCTTG ACCTTGTGAT 840
367 CTGCCTGCCT CGGCCTCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC 900
369 TATTTTAAAT TTTTGTGTTG TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA 960
371 ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT 1020
373 CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCCGCTAA TTTTGTATT 1080
375 TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAACCTC TGACCTCAGG 1140
377 TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GCGGTGACGC CTCACCCAGC 1200
379 CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG 1260
381 GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAATGAGC CACAACACCC AGCCAGTCAC 1320
383 ATTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG 1380
385 AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT 1418

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387 (2) INFORMATION FOR SEQ ID NO: 5:

389 (i) SEQUENCE CHARACTERISTICS:

390 (A) LENGTH: 22 base pairs

391 (B) TYPE: nucleic acid

392 (C) STRANDEDNESS: single

VERIFICATION SUMMARY

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DATE: 10/18/2001

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]